



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Breece, Tim
Hayenga, Kirk
Rinderknecht, Ernst
Vandlen, Richard
Yansura, Daniel

(ii) TITLE OF INVENTION: PROCESS FOR PRODUCING RELAXIN

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/080,354
(B) FILING DATE: 21-JUN-1993
(C) CLASSIFICATION:

C' (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Walter H.
(B) REGISTRATION NUMBER: 24,190
(C) REFERENCE/DOCKET NUMBER: A-58117/WH

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ser Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val
1 5 10 15

Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser
20 25

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr
1 5 10 15

Lys Arg Ser Leu Ala Arg Phe Cys
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	AAA	AAG	AAT	ATC	GCA	TTT	CTT	CTT	AAA	CGG	GAC	TCA	TGG	ATG	GAG	48
Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Lys	Arg	Asp	Ser	Trp	Met	Glu	
1				5					10					15		
GAA	GTT	ATT	AAA	TTA	TGC	GGC	CGC	GAA	TTA	GTT	CGC	GCG	CAG	ATT	GCC	96
Glu	Val	Ile	Lys	Leu	Cys	Gly	Arg	Glu	Leu	Val	Arg	Ala	Gln	Ile	Ala	
			20					25					30			

ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC ACT GGT TAT GGT	144
Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly	
35 40 45	
TCT CGA AAA AAG AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC	192
Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys	
50 55 60	
CAT GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC	231
His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 593 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 431..586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA 60

GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA 120

AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG 180

GTTGATTGAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA 240

CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300

AAAAGTTAAT CTTTTCACAA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT 360

TGTTTTTATT TTTTAATGTA TTTGTACGCA AGTTCACGTA AAAAGGGTAT CTAGAGGTTG 420

AGGTGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC 469

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe

1 5 10

GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA GAC TCA TGG ATG GAG GAA 517

Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu

15 20 25

GTT ATT AAA TTA TGC GGC CGC GAA TTG GTA CGC GCG CAA ATA GCG ATA 565

Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile

30 35 40 45

TGC GGT ATG AGT ACA TGG AGT TGAAGAA 593

Cys Gly Met Ser Thr Trp Ser

50

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 438..1238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA 60
 GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA 120
 AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG 180
 GTTGATTCAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA 240
 CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300
 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT 360
 TGTTTTTTATT TTTTAATGTA TTTGTAAC TAACGCAAGT TCACGTAAAA AGGGTATCTA 420
 GAGGTTGAGG TGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT 470
 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser
 1 5 10
 ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TCA GGC ACT ACA 518
 Met Phe Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr
 15 20 25
 AAT ACT GTG GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT TTC AAG 566
 Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys
 30 35 40
 ACA ATT TTG GAG TGG GAA CCC AAA CCC GTC AAT CAA GTC TAC ACT GTT 614
 Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val
 45 50 55
 CAA ATA AGC ACT AAG TCA GGA GAT TGG AAA AGC AAA TGC TTT TAC ACA 662
 Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr
 60 65 70 75
 ACA GAC ACA GAG TGT GAC CTC ACC GAC GAG ATT GTG AAG GAT GTG AAG 710
 Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys
 80 85 90
 CAG ACG TAC TTG GCA CGG GTC TTC TCC TAC CCG GCA GGG AAT GTG GAG 758
 Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu
 95 100 105
 AGC ACC GGT TCT GCT GGG GAG CCT CTG TAT GAG AAC TCC CCA GAG TTC 806
 Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe
 110 115 120
 ACA CCT TAC CTG GAG ACA AAC CTC GGA CAG CCA ACA ATT CAG AGT TTT 854
 Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe
 125 130 135
 GAA CAG GTG GGA ACA AAA GTG AAT GTG ACC GTA GAA GAT GAA CGG ACT 902
 Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr
 140 145 150 155
 TTA GTC AGA AGG AAC AAC ACT TTC CTA AGC CTC CGG GAT GTT TTT GGC 950
 Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly
 160 165 170

c' cont.

AAG GAC TTA ATT TAT ACA CTT TAT TAT TGG AAA TCT TCA AGT TCA GGA 998
 Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly
 175 180 185
 AAG AAA ACA GCC AAA ACA AAC ACT AAT GAG TTT TTG ATT GAT GTG GAT 1046
 Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp
 190 195 200
 AAA GGA GAA AAC TAC TGT TTC AGT GTT CAA GCA GTG ATT CCC TCC CGA 1094
 Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg
 205 210 215
 ACA GTT AAC CGG AAG AGT ACA GAC AGC CCG GTA GAG TGT ATG GGC CAG 1142
 Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln
 220 225 230 235
 GAG AAA GGC CAA TTC AGA GAA ATA TTC TAC ATC ATT GGA GCT GTG GTA 1190
 Glu Lys Gly Gln Phe Arg Glu Ile Phe Tyr Ile Ile Gly Ala Val Val
 240 245 250
 TTT GTG GTC ATC ATC CTT GTC ATC ATC CTG GCT ATA TCT CTA CAC TAAAATTCTC 1245
 Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile Ser Leu His
 255 260 265
 ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG TTAAATTGCT 1305
 AACGCAGTCA GGCACCGTGT ATGAAATCTA ACAATGCGCT CATCGTCATC CTCGGCACCG 1365
 TCACCCTGGA TGCTGTAGGC ATAGGCTTGG TTATGCCGGT ACTGCCGGGC CTCTTGCGGG 1425
 ATATCGTCCA TTCCGACAGC ATCGCCAGTC ACTATGGCGT GCTCCTAGCG CTATATGCGT 1485
 TGATGCAATT TCTAT 1500

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Lys Asn Ile Ala Phe Leu Leu Arg Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Lys Asn Ile Ala Phe Leu Leu Arg Arg
 1 5 10

C'
cont.

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5..42
- (D) OTHER INFORMATION: /note= "Complementary
double-stranded binding between bases 5 and 42 to
SEQ ID NO:16. "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTAGAATTAT GAAAAAGAAT ATCGCATTTT TTCTTAAACG GG

42

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 4..41
- (D) OTHER INFORMATION: /note= "Complementary
double-stranded binding between bases 4 and 41 to
SEQ ID NO:15. "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AGTCCCGTTT AAGAAGAAAT GCGATATTCT TTTTCATAAT T

41

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5..42
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 42 to SEQ ID NO:18."

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTAGAATT ATG TTC CCA GCT ATG CCT CTA TCT AGT AAA CGG G
Met Phe Pro Ala Met Pro Leu Ser Ser Lys Arg
1 5 10

42

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 4..41
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 4 and 41 to SEQ ID NO:17."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTCCCGTTT ACTAGATAGA GGCATAGCTG GGAACATAAT T

41

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Phe Pro Ala Met Pro Leu Ser Ser Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 5..64

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5..64
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 64 to SEQ ID NO:21."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGCG CAG ATT GCC ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC 49
Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro
1 5 10 15
ACT GGT TAT GGT TCT 64
Thr Gly Tyr Gly Ser
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 3..62
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 3 and 62 to SEQ ID NO:20."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGAGAACCAT AACCAGTGGG TTTCCTTTTG CTCCAGGTGC TCATGCCGCA AATGGCAATC 60
TG 62

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr
1 5 10 15
Gly Tyr Gly Ser
20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5..50
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 50 with SEQ ID NO:24."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCACTCTG TCGGGTGCTG AACTGGTTGA CGCTCTGCAG TTTGTTTGCG

50

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6..50
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 6 and 50 with SEQ ID NO:23."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCACCGCAA ACAAACTGCA GAGCGTCAAC CAGTTCAGCA CCGCAAGAGT

50

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 1 and 55 with SEQ ID NO:26."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTCCCCGAAA CTCTGTGCGG TGCTGAACTG GTTGACGCTC TGCAGTTTGT TTGCG

55

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs

C'
cont.

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6..64
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 6 and 64 with SEQ ID NO:25."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCACCGCAA ACAAACTGCA GAGCGTCAAC CAGTTCAGCA CCGCACAGAG TTTCGGGACC 60
TGCA 64

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5..84
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 84 with SEQ ID NO:28."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGAATTAT GATGATTACT CTGCGCAAAC TTCCTCTGGC GGTGCGCGTC GCAGCGGGCG 60
TAATGTCTGC TCAGGCCATG GCCA 84

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5..84
- (D) OTHER INFORMATION: /note= "Complementary double-stranded binding between bases 5 and 84 with SEQ ID NO:27."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATCTGGCCA TGGCCTGAGC AGACATTACG CCCGCTGCGA CGGCAACCGC CAGAGGAAGT 60
TTGCGCAGAG TAATCATCAT AATT 84

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: /note= "Complementary
double-stranded binding between bases 1 and 52
with SEQ ID NO:30."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAACTCTACA GTGCATTGGC TAATAAATGT TGCCATGTTG GTTGTACCAA AA

52

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 5..56
- (D) OTHER INFORMATION: /note= "Complementary
double-stranded binding between bases 5 and 56
with SEQ ID NO:29."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCTTTTGG TACAACCAAC ATGGCAACAT TTATTAGCCA ATGCACTGTA GAGTTGTGCA

60

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu
1 5 10 15
Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala
20 25 30
Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly
35 40 45
Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys
50 55 60
His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys
65 70 75

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC ATT TGC GGC ATG AGC	47
Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser	
1 5 10 15	
ACC TGG AGC AAA AGG TCT CTG AGC CAG GAA GAT GCT CCT CAG ACA CCT	95
Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln Thr Pro	
20 25 30	
AGA CCA GTG GCA GAA ATT GTG CCA TCC TTC ATC AAC AAA GAT ACA GAA	143
Arg Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp Thr Glu	
35 40 45	
ACC ATA AAT ATG ATG TCA GAA TTT GTT GCT AAT TTG CCA CAG GAG CTG	191
Thr Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln Glu Leu	
50 55 60	
AAG TTA ACC CTG TCT GAG ATG CAG CCA GCA TTA CCA CAG CTA CAA CAA	239
Lys Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu Gln Gln	
65 70 75	
CAT GTA CCT GTA TTA AAA GAT TCC AGT CTT CTC TTT GAA GAA TTT AAG	287
His Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu Phe Lys	
80 85 90 95	
AAA CTT ATT CGC AAT AGA CAA AGT GAA GCC GCA GAC AGC AGT CCT TCA	335
Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser Pro Ser	
100 105 110	
GAA TTA AAA TAC TTA GGC TTG GAT ACT CAT TCT CGA AAA AAG AGA CAA	383
Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys Arg Gln	
115 120 125	
CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC CAT GTT GGT TGT ACC AAA	431
Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr Lys	
130 135 140	
AGA TCT CTT GCT AGA TTT TGC TGAGATGAAG CTAATTGTGC ACATCTCGTA	482
Arg Ser Leu Ala Arg Phe Cys	
145 150	
TAATATTCAC ACATATTCTT AATGACATTT CACTGATGCT TCTATCAGGT CAATTCTCAT	542
GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT TATCACAGTT AAATTGCTAA	602
CGCAGTCAGG CACCGTGTAT GAAATCTAAC AATGCGCTCA TCGTCATCCT CGGCACCGTC	662
ACCCTGGATG CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT	722
ATCGTCCATT CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG	782
ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG CCGCCGCCCA	842
GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG CGATCATGGC GACCACACCC	902
GTCCTGTGGA TCC	915

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr
 1 5 10 15
 Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln Thr Pro Arg
 20 25 30
 Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp Thr Glu Thr
 35 40 45
 Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln Glu Leu Lys
 50 55 60
 Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu Gln Gln His
 65 70 75 80
 Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu Phe Lys Lys
 85 90 95
 Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser Pro Ser Glu
 100 105 110
 Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys Arg Gln Leu
 115 120 125
 Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr Lys Arg
 130 135 140
 Ser Leu Ala Arg Phe Cys
 145 150

C'
cont.

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
 1 5 10 15
 Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu Val Ile Lys
 20 25 30
 Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met
 35 40 45
 Ser Thr Trp Ser
 50

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
 1 5 10 15
 Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr Asn Thr Val Ala Ala
 20 25 30
 Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp
 35 40 45
 Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys
 50 55 60
 Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys
 65 70 75 80
 Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala
 85 90 95
 Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala
 100 105 110
 Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu
 115 120 125
 Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr
 130 135 140
 Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn
 145 150 155 160
 Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr
 165 170 175
 Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys
 180 185 190
 Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr
 195 200 205
 Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys
 210 215 220
 Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Gln Phe
 225 230 235 240
 Arg Glu Ile Phe Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile
 245 250 255
 Leu Val Ile Ile Leu Ala Ile Ser Leu His
 260 265

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 7..297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGCTT ATG AAA TCT AAC AAT GCG CTC ATC GTC ATC CTC GGC ACC GTC Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val 1 5 10	48
ACC CTG GAT GCT GTA GGC ATA GGC TTG GTT ATG CCG GTA CTG CCG GGC Thr Leu Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly 15 20 25 30	96
CTC TTG CGG GAT ATC GTC CAT TCC GAC AGC ATC GCC AGT CAC TAT GGC Leu Leu Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly 35 40 45	144
GTG CTG CTA GCG CTA TAT GCG TTG ATG CAA TTT CTA TGC GCA CCC GTT Val Leu Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val 50 55 60	192
CTC GGA GCA CTG TCC GAC CGC TTT GGC CGC CGC CCA GTC CTG CTC GCT Leu Gly Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala 65 70 75	240
TCG CTA CTT GGA GCC ACT ATC GAC TAC GCG ATC ATG GCG ACC ACA CCC Ser Leu Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro 80 85 90	288
GTC CTG TGG ATCC Val Leu Trp 95	301

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val Thr Leu
1 5 10 15

Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly Leu Leu
20 25 30

Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly Val Leu
35 40 45

Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val Leu Gly
50 55 60

Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala Ser Leu
65 70 75 80

Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro Val Leu
85 90 95

Trp

C1
wed.